SEQUENCE LISTING

<110> ASAHI KASEI KABUSHIKI KAISHA
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      ONO, Mitsuharu
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<120> Novel receptor protein and method for the diagnosis of an
      inflammatory disease by using the same

<130> 99-1043

<150> JP 10-249752
<151> 1998-09-03

<150> JP 11-070800
<151> 1999-03-16

<150> PCT/JP99/04801
<151> 1999-09-03

<160> 12

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tcg gac cgc cct gtg gac tgc ctg gat ggc gcc tgc ctg gcc atc gac   96
Ser Asp Arg Pro Val Asp Cys Leu Asp Gly Ala Cys Leu Ala Ile Asp
                20   25   30
ccg ctg cgc gtg gcc ccg ctc cca ctg tat gcc gcc atc ttc ctg gtg   144
Pro Leu Arg Val Ala Pro Leu Pro Leu Tyr Ala Ala Ile Phe Leu Val
            35   40   45
ggg gtg ccg ggc aat gcc atg gtg gcc tgg gtg gct ggg aag gtg gcc   192
Gly Val Pro Gly Asn Ala Met Val Ala Trp Val Ala Gly Lys Val Ala
        50   55   60
cgc cgg agg gtg ggt gcc acc tgg ttg ctc cac ctg gcc gtg gcg gat   240
Arg Arg Arg Val Gly Ala Thr Trp Leu Leu His Leu Ala Val Ala Asp

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ttg ctg tgc tgt ttg tct ctg ccc atc ctg gca gtg ccc att gcc cgt    288
Leu Leu Cys Cys Leu Ser Leu Pro Ile Leu Ala Val Pro Ile Ala Arg
                        85                          90                          95
gga ggc cac tgg ccg tat ggt gca gtg ggc tgt cgg gcg ctg ccc tcc    336
Gly Gly His Trp Pro Tyr Gly Ala Val Gly Cys Arg Ala Leu Pro Ser
                    100                         105                         110
atc atc ctg ctg acc atg tat gcc agc gtc ctg ctc ctg gca gct ctc    384
Ile Ile Leu Leu Thr Met Tyr Ala Ser Val Leu Leu Leu Ala Ala Leu
                115                         120                         125
agt gcc gac ctc tgc ttc ctg gct ctc ggg cct gcc tgg tgg tct acg    432
Ser Ala Asp Leu Cys Phe Leu Ala Leu Gly Pro Ala Trp Trp Ser Thr
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gtt cag cgg gcg tgc ggg gtg cag gtg gcc tgt ggg gca gcc tgg aca    480
Val Gln Arg Ala Cys Gly Val Gln Val Ala Cys Gly Ala Ala Trp Thr
145                         150                         155                         160
ctg gcc ttg ctg ctc acc gtg ccc tcc gcc atc tac cgc cgg ctg cac    528
Leu Ala Leu Leu Leu Thr Val Pro Ser Ala Ile Tyr Arg Arg Leu His
                    165                         170                         175
cag gag cac ttc cca gcc cgg ctg cag tgt gtg gtg gac tac ggc ggc    576
Gln Glu His Phe Pro Ala Arg Leu Gln Cys Val Val Asp Tyr Gly Gly
                180                         185                         190
tcc tcc agc acc gag aat gcg gtg act gcc atc cgg ttt ctt ttt ggc    624
Ser Ser Ser Thr Glu Asn Ala Val Thr Ala Ile Arg Phe Leu Phe Gly
            195                         200                         205
ttc ctg ggg ccc ctg gtg gcc gtg gcc agc tgc cac agt gcc ctc ctg    672
Phe Leu Gly Pro Leu Val Ala Val Ala Ser Cys His Ser Ala Leu Leu
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tgc tgg gca gcc cga cgc tgc cgg ccg ctg ggc aca gcc att gtg gtg    720
Cys Trp Ala Ala Arg Arg Cys Arg Pro Leu Gly Thr Ala Ile Val Val
225                         230                         235                         240
ggg ttt ttt gtc tgc tgg gca ccc tac cac ctg ctg ggg ctg gtg ctc    768
Gly Phe Phe Val Cys Trp Ala Pro Tyr His Leu Leu Gly Leu Val Leu
                    245                         250                         255
act gtg gcg gcc ccg aac tcc gca ctc ctg gcc agg gcc ctg cgg gct    816
Thr Val Ala Ala Pro Asn Ser Ala Leu Leu Ala Arg Ala Leu Arg Ala
                260                         265                         270
gaa ccc ctc atc gtg ggc ctt gcc ctc gct cac agc tgc ctc aat ccc    864
Glu Pro Leu Ile Val Gly Leu Ala Leu Ala His Ser Cys Leu Asn Pro
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atg ctc ttc ctg tat ttt ggg agg gct caa ctc cgc cgg tca ctg cca    912
Met Leu Phe Leu Tyr Phe Gly Arg Ala Gln Leu Arg Arg Ser Leu Pro
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gct gcc tgt cac tgg gcc ctg agg gag tcc cag ggc cag gac gaa agt    960
Ala Ala Cys His Trp Ala Leu Arg Glu Ser Gln Gly Gln Asp Glu Ser
305                         310                         315                         320
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gtg tag
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<210> 2
<211> 337
<212> PRT
<213> Homo sapiens

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Pro	Leu	Arg	Val	Ala	Pro	Leu	Pro	Leu	Tyr	Ala	Ala	Ile	Phe	Leu	Val
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Arg	Arg	Arg	Val	Gly	Ala	Thr	Trp	Leu	Leu	His	Leu	Ala	Val	Ala	Asp
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Leu	Leu	Cys	Cys	Leu	Ser	Leu	Pro	Ile	Leu	Ala	Val	Pro	Ile	Ala	Arg
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Ser	Ala	Asp	Leu	Cys	Phe	Leu	Ala	Leu	Gly	Pro	Ala	Trp	Trp	Ser	Thr
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Val	Gln	Arg	Ala	Cys	Gly	Val	Gln	Val	Ala	Cys	Gly	Ala	Ala	Trp	Thr
145				150					155						160
Leu	Ala	Leu	Leu	Leu	Thr	Val	Pro	Ser	Ala	Ile	Tyr	Arg	Arg	Leu	His
			165					170					175		
Gln	Glu	His	Phe	Pro	Ala	Arg	Leu	Gln	Cys	Val	Val	Asp	Tyr	Gly	Gly
			180					185					190		
Ser	Ser	Ser	Thr	Glu	Asn	Ala	Val	Thr	Ala	Ile	Arg	Phe	Leu	Phe	Gly
		195					200					205			
Phe	Leu	Gly	Pro	Leu	Val	Ala	Val	Ala	Ser	Cys	His	Ser	Ala	Leu	Leu
	210					215					220				
Cys	Trp	Ala	Ala	Arg	Arg	Cys	Arg	Pro	Leu	Gly	Thr	Ala	Ile	Val	Val
225					230					235					240
Gly	Phe	Phe	Val	Cys	Trp	Ala	Pro	Tyr	His	Leu	Leu	Gly	Leu	Val	Leu
			245					250					255		
Thr	Val	Ala	Ala	Pro	Asn	Ser	Ala	Leu	Leu	Ala	Arg	Ala	Leu	Arg	Ala
		260					265					270			
Glu	Pro	Leu	Ile	Val	Gly	Leu	Ala	Leu	Ala	His	Ser	Cys	Leu	Asn	Pro
	275					280					285				
Met	Leu	Phe	Leu	Tyr	Phe	Gly	Arg	Ala	Gln	Leu	Arg	Arg	Ser	Leu	Pro
290					295					300					
Ala	Ala	Cys	His	Trp	Ala	Leu	Arg	Glu	Ser	Gln	Gly	Gln	Asp	Glu	Ser

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<212> DNA
<213> Homo sapiens

<400> 3

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cggaccgccc tgtggactgc ctggatggcg cctgcctggc catcgacccg ctgcgcgtgg  180
ccccgctccc actgtatgcc gccatcttcc tggtgggggt gccgggcaat gccatggtgg  240
cctgggtggc tgggaaggtg gcccgccgga gggtgggtgc cacctggttg ctccacctgg  300
ccgtggcgga tttgctgtgc tgtttgtctc tgcccatcct ggcagtgccc attgcccgtg  360
gaggccactg gccgtatggt gcagtgggct gtcgggcgct gccctccatc atcctgctga  420
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tcgggcctgc ctggtggtct acggttcagc gggcgtgcgg ggtgcaggtg cctgtgggg  540
cagcctggac actggccttg ctgctcaccg tgccctccgc catctaccgc cggctgcacc  600
aggagcactt cccagcccgg ctgcagtgtg tggtggacta cggcggctcc tccagcaccg  660
agaatgcggt gactgccatc cggtttcttt ttggcttcct ggggcccctg gtggccgtgg  720
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tgtaggctgg agagacattg tgggtgtgta tcttcttatc tcatttcaca agactggctt 1140
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tgaccaaaac agacacaaat cctgccc                                    1287
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<210> 4
<211> 1287
<212> DNA
<213> Homo sapiens

<400> 4

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ttgagctcct ggatccagct atgcctgaag ccagtcttgt gaaatgagat aagaagatac  180
acacccacaa tgtctctcca gcctacacct ccatctccga gaccaggtca tggctggtgg  240
atttcttgct gtccacactt tcgtcctggc cctgggactc cctcagggcc cagtgacagg  300
cagctggcag tgaccggcgg agttgagccc tcccaaaata caggaagagc atgggattga  360
ggcagctgtg agcgagggca aggcccacga tgaggggttc agcccgcagg ccctggcca  420
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ggagtgcgga gttcggggcc gccacagtga gcaccagccc cagcaggtgg tagggtgccc    480
agcagacaaa aaaccccacc acaatggctg tgcccagcgg ccggcagcgt cgggctgccc    540
agcacaggag ggcactgtgg cagctggcca cggccaccag gggccccagg aagccaaaaa    600
gaaaccggat ggcagtcacc gcattctcgg tgctggagga gccgccgtag tccaccacac    660
actgcagccg ggctgggaag tgctcctggt gcagccggcg gtagatggcg gagggcacgg    720
tgagcagcaa ggccagtgtc caggctgccc cacaggccac ctgcaccccg cacgcccgct    780
gaaccgtaga ccaccaggca ggcccgagag ccaggaagca gaggtcggca ctgagagctg    840
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acaaacagca cagcaaatcc gccacggcca ggtggagcaa ccaggtggca cccaccctcc   1020
ggcgggccac cttcccagcc acccaggcca ccatggcatt gcccggcacc cccaccagga   1080
agatggcggc atacagtggg agcggggcca cgcgcagcgg gtcgatggcc aggcaggcgc   1140
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agatttgtcc agcacgtggc acacagg                                      1287


<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> modified base
<222> 18
<223> i

<220>
<221> modified base
<222> 22
<223> i

<220>
<221> modified base
<222> 24
<223> i

<220>
<223> Degenerative PCR primer designed based on the seq of
conventional
      7-pass transmembrane receptor proteins which are considered to
      participate in the proliferation of melanoma


<400> 5
atcttaagct tgaacctngc cntngcdgac                                      30


<210> 6
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<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> misc difference
<222> 21
<223> a, g, c or t

<220>
<221> modified base
<222> 22
<223> i

<220>
<221> modified base
<222> 28
<223> i

<220>
<223> Degenerative PCR primer designed based on the seq of conventional
    7-pass transmembrane receptor proteins which are considered to
    participate in the proliferation of melanoma

<400> 6
cccaacgaat tcrtagatsa nnggrttnav rca   33

<210> 7
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer used for constructing the recombinant DNA
    containing C5L2 gene; primer has a seq obtained by adding spacer
    gggg and HindIII site aagctt to the 5'-end of a 22-nucleotide
    seq corresponding to the 1st (a) to 22nd (t) of SEQ ID NO:1

<400> 7
ggggaagctt atggggaacg attctgtcag ct   32

<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer used for constructing the recombinant DNA
      containing C5L2 gene; primer has a seq obtained by adding spacer
      ggga and SacII site ccgcgg to the 5'-end of a 20-nucleotide
      seq corresponding to the 206th (c) to 225th (a) of SEQ ID NO:4

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gggaccgcgg cacctccatc tccgagacca   30

<210> 9
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer used in RT-PCR performed for amplifying
      C5L2 gene

<400> 9
atcatcctgc tgaccatgta tgccag   26

<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer used in RT-PCR performed for amplifying
      C5L2 gene

<400> 10
aaccggatgg cagtcaccgc attct   25

<210> 11
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer used in RT-PCR performed for amplifying G3PDH
      (glyceraldehyde 3-phosphate dehydrogenase) gene

<400> 11
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<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic primer used in RT-PCR performed for amplifying G3PDH
      (glyceraldehyde 3-phosphate dehydrogenase) gene

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